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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/897,425

DATE: 10/19/2001

TIME: 12:40:10

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3 <110> APPLICANT: MOLONEY, MAURICE M.
 4 DALMIA, BIPIN K.
 6 <120> TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
 7 PROTEINS ON OIL BODIES
 9 <130> FILE REFERENCE: 034547/0106
 11 <140> CURRENT APPLICATION NUMBER: 09/897,425
 12 <141> CURRENT FILING DATE: 2001-07-03
 14 <150> PRIOR APPLICATION NUMBER: 09/210,843
 15 <151> PRIOR FILING DATE: 1998-12-18
 17 <150> PRIOR APPLICATION NUMBER: 08/846,021
 18 <151> PRIOR FILING DATE: 1997-04-25
 20 <150> PRIOR APPLICATION NUMBER: 08/366,783
 21 <151> PRIOR FILING DATE: 1994-12-30
 23 <150> PRIOR APPLICATION NUMBER: 08/142,418
 24 <151> PRIOR FILING DATE: 1993-11-16
 26 <150> PRIOR APPLICATION NUMBER: 07/659,835
 27 <151> PRIOR FILING DATE: 1991-02-22
 29 <160> NUMBER OF SEQ ID NOS: 55
 31 <170> SOFTWARE: PatentIn Ver. 2.1
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 1800
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Arabidopsis thaliana
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 39 <221> NAME/KEY: CDS
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 44 <222> LOCATION: (1462)..(1626)
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 51 tegtogggtc cttgggcgat tgcggcgga gatgggtcag cttgggcttg aggacgagac 180
 53 ccgaatcgag tctgttgaaa ggttggtcat tgggatttgt atacggagat tggtcgtcga 240
 55 gaggtttgag ggaaaggaca aatgggtttg gctctggaga aagagagtgc ggcttttagag 300
 57 agagaattga gaggtttaga gagagatgcg gcggcgatga cgggaggaga gacgacgagg 360
 59 acctgcatta tcaaagcagt gacgtggtga aatttggaac ttttaagagg cagatagatt 420
 61 tattatttgt atccattttc ttcatgttgc tagaatgtcg cggaacaaat tttaaaacta 480
 63 aatcctaaat ttttctaatt ttgttgccaa tagtgatgat gtgggccgta tagaaggaat 540
 65 ctattgaagg cccaaacca tactgacgag cccaaagggt cgttttgcgt tttatgtttc 600
 67 ggttcgtatc caacgccaca ttctgagcta ggcaaaaaac aaacgtgtct ttgaatagac 660
 69 tcctctcgtt aacacatgca gcggctgcat ggtgacgcca ttaacacgtg gcctacaatt 720
 71 gcatgatgtc tccattgaca cgtgacttct cgtctccttt cttaatatat ctaacaaaca 780
 73 ctctacctc ttccaaaata tatacacatc tttttgatca atctctcatt caaatctca 840
 75 ttctctctag taaacaagaa caaaaaa atg gcg gat aca gct aga gga acc cat 894
 76 Met Ala Asp Thr Ala Arg Gly Thr His
 77 1 5

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79 cac gat atc atc ggc aga gac cag tac ccg atg atg ggc cga gac cga 942
80 His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg
81 10 15 20 25
83 gac cag tac cag atg tcc gga cga gga tct gac tac tcc aag tct agg 990
84 Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg
85 30 35 40
87 cag att gct aaa gct gca act gct gtc aca gct ggt ggt tcc ctc ctt 1038
88 Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu
89 45 50 55
91 gtt ctc tcc agc ctt acc ctt gtt gga act gtc ata gct ttg act gtt 1086
92 Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val
93 60 65 70
95 gca aca cct ctg ctc gtt atc ttc agc cca atc ctt gtc ccg gct ctc 1134
96 Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu
97 75 80 85
99 atc aca gtt gca ctc ctc atc acc ggt ttt ctt tcc tct gga ggg ttt 1182
100 Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe
101 90 95 100 105
103 ggc att gcc gct ata acc gtt ttc tct tgg att tac aag taagcacaca 1231
104 Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile Tyr Lys
105 110 115
107 tttatcatct tacttcataa ttttgtgcaa tatgtgcatg catgtgttga gccagtagct 1291
109 ttggatcaat ttttttggtc gaataacaaa tgtaacaata agaaattgca aattctaggg 1351
111 aacatttggt taactaaata cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat 1411
113 catctatata ggtaaaatgc ttggtatgat acctattgat tgtgaatagg tac gca 1467
114 Tyr Ala
115 120
117 acg gga gag cac cca cag gga tca gac aag ttg gac agt gca agg atg 1515
118 Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala Arg Met
119 125 130 135
121 aag ttg gga agc aaa gct cag gat ctg aaa gac aga gct cag tac tac 1563
122 Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr
123 140 145 150
125 gga cag caa cat act ggt ggg gaa cat gac cgt gac cgt act cgt ggt 1611
126 Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr Arg Gly
127 155 160 165
129 ggc cag cac act act taagttaccc cactgatgtc atcgtcatag tccaataact 1666
130 Gly Gln His Thr Thr
131 170
133 ccaatgtcgg ggagttagtt tatgaggaat aaagtgttta gaatttgatc agggggagat 1726
135 aataaaagcc gagtttgaat ctttttggtta taagtaatgt ttatgtgtgt ttctatatgt 1786
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143 <213> ORGANISM: Arabidopsis thaliana
145 <400> SEQUENCE: 2
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149 Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
150          20          25          30
152 Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
153          35          40          45
155 Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
156          50          55          60
158 Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
159 65          70          75          80
161 Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
162          85          90          95
164 Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
165          100          105          110
167 Phe Ser Trp Ile Tyr Lys
168          115
171 <210> SEQ ID NO: 3
172 <211> LENGTH: 55
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174 <213> ORGANISM: Arabidopsis thaliana
176 <400> SEQUENCE: 3
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178 1          5          10          15
180 Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
181          20          25          30
183 Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
184          35          40          45
186 Arg Gly Gly Gln His Thr Thr
187          50          55
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192 <211> LENGTH: 564
193 <212> TYPE: DNA
194 <213> ORGANISM: Brassica napus
196 <220> FEATURE:
197 <221> NAME/KEY: CDS
198 <222> LOCATION: (1)..(561)
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203 1          5          10          15
205 tat ccc cga gac cga gac cag tat tct atg atc ggt cga gac cgt gac 96
206 Tyr Pro Arg Asp Arg Asp Gln Tyr Ser Met Ile Gly Arg Asp Arg Asp
207          20          25          30
209 cag tac tct atg atg ggc cga gac cga gac cag tac aac atg tat ggt 144
210 Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
211          35          40          45
213 cga gac tac tcc aag tct aga cag att gct aag gct gtt acc gca gtc 192
214 Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
215          50          55          60
217 acg gcg ggt ggg tcc ctc ctt gtc ctc tcc agt ctc acc ctt gtt ggt 240
218 Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly

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219 65          70          75          80
221 act gtc att gct ttg act gtt gcc act cca ctc ctc gtt atc ttt agc 288
222 Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
223          85          90          95
225 cca atc ctc gtg ccg gct ctc atc acc gta gca ctt ctc atc act ggc 336
226 Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
227          100          105          110
229 ttt ctc tcc tct ggt ggg ttt gcc att gca gct ata acc gtc ttc tcc 384
230 Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
231          115          120          125
233 tgg atc tat aag tac gca acg gga gag cac cca cag ggg tca gat aag 432
234 Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
235          130          135          140
237 ttg gac agt gca agg atg aag ctg gga acc aaa gct cag gat att aaa 480
238 Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
239 145          150          155          160
241 gac aga gct caa tac tac gga cag caa cat aca ggt ggt gag cat gac 528
242 Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
243          165          170          175
245 cgt gac cgt act cgt ggt ggc cag cac act act taa 564
246 Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
247          180          185
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251 <211> LENGTH: 187
252 <212> TYPE: PRT
253 <213> ORGANISM: Brassica napus
255 <400> SEQUENCE: 5
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262 Gln Tyr Ser Met Met Gly Arg Asp Arg Asp Gln Tyr Asn Met Tyr Gly
263          35          40          45
265 Arg Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Val Thr Ala Val
266          50          55          60
268 Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly
269 65          70          75          80
271 Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser
272          85          90          95
274 Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly
275          100          105          110
277 Phe Leu Ser Ser Gly Gly Phe Ala Ile Ala Ala Ile Thr Val Phe Ser
278          115          120          125
280 Trp Ile Tyr Lys Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys
281          130          135          140
283 Leu Asp Ser Ala Arg Met Lys Leu Gly Thr Lys Ala Gln Asp Ile Lys
284 145          150          155          160
286 Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp
287          165          170          175

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296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: Fragment of
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302      gene
304 <220> FEATURE:
305 <221> NAME/KEY: CDS
306 <222> LOCATION: (850)..(1203)
308 <220> FEATURE:
309 <221> NAME/KEY: CDS
310 <222> LOCATION: (1444)..(2724)
312 <400> SEQUENCE: 6
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315 ggcgcaaat gccggaatt ctgacctgaa gacggaacat catcgctcggg tccttggggcg 120
317 attgcggcg aagatgggtc agcttgggct tgaggacgag acccgaaatcg agtctgttga 180
319 aagggtgttc attgggattt gtatacggag attggtcgtc gagagggttg agggaaagga 240
321 caaatgggtt tggctctgga gaaagagagt gcggctttag agagagaatt gagaggttta 300
323 gagagagatg cggcggcgat gacgggagga gagacgacga ggacctgcat tatcaaagca 360
325 gtgacgtggt gaaatttga acttttaaga ggcagataga tttattattt gtatccattt 420
327 tcttcattgt tctagaatgt cgcggaacaa attttaaaac taaatcctaa atttttctaa 480
329 ttttgttgcc aatagtggat atgtgggccc tatagaagga atctattgaa ggcccaaacc 540
331 catactgacg agcccaaagg ttcgttttgc gttttatggt tcggttcgat gccaacgcca 600
333 cattctgagc taggcacaaa acaaacgtgt ctttgaatag actcctctcg ttaacacatg 660
335 cagcggctgc atggtgacgc cattaacacg tggcctacaa ttgcatgatg tctccattga 720
337 cacgtgactt ctcgctctct ttcttaatat atctaacaaa cactcctacc tcttccaaaa 780
339 tatatacaca tctttttgat caatctotca ttcaaatct cattctctct agtaaacaag 840
341 aacaaaaaaa atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc 891
342      Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly
343      1      5      10
345 aga gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg 939
346 Arg Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met
347 15      20      25      30
349 tcc gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct 987
350 Ser Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala
351      35      40      45
353 gca act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt 1035
354 Ala Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu
355      50      55      60
357 acc ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc 1083
358 Thr Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu
359      65      70      75
361 gtt atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc 1131
362 Val Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu
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VERIFICATION SUMMARY

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